**APPENDIX A - CLAIM AMENDMENTS**
**INCLUDING NOTATIONS TO INDICATE CHANGES MADE**
**Serial No.:** 09/981,286
**Docket No.:** 265.00260101

Amendments to the following are indicated by underlining what has been added and bracketing what has been deleted.

**In the Claims**

For convenience, all pending claims are shown below.

1. A collection of polypeptides comprising at least two polypeptides, each polypeptide comprising a fragment of SEQ ID NO:1 beginning at any amino acid from about 119 to about 124 and ending at any amino acid from about 258 to about 275, wherein at least two consecutive amino acids within the regions of amino acids 129-137, or amino acids 182-189, or amino acids 257-264 as depicted at SEQ ID NO:1 are replaced by an amino acid sequence comprising $Xaa_n$, wherein n is from about 5 to about 21, and each Xaa is independently a random amino acid.

2. The collection of claim 1 wherein each member of the collection further comprises a cell-permeant region fused to the amino terminal end of the polypeptide.

3. The collection of claim 2 wherein the cell-permeant region comprises an amino acid sequence selected from the group consisting of YGRKKRRQRRR (SEQ ID NO:2), RQIKIWFQNRRMKWKK (SEQ ID NO:3), RQIKIWFPNRRMKWKK (SEQ ID NO:4), and RQPKIWFPNRRPKWKK (SEQ ID NO:5).

4. The collection of claim 1 wherein the collection comprises a polypeptide selected from the group consisting of SEQ ID NO:33 and SEQ ID NO:34.

5. A cell comprising a member of the collection of claim 1.

6. A population of cells comprising two or more cells, wherein each member of the population comprises one polypeptide of the collection of claim 1.

7. A collection of polypeptides wherein the collection comprises a polypeptide selected from the group consisting of SEQ ID NO:33 and SEQ ID NO:34.

8. A polypeptide selected from the group consisting of

an amino acid sequence SEQ ID NO:2 fused to an amino terminal end of a fragment of SEQ ID NO:1 beginning at any amino acid from about 119 to about 124 and ending at any amino acid from about 258 to about 275,

wherein at least two consecutive amino acids within the regions of amino acids 129-137, or amino acids 182-189, or amino acids 257-264 as depicted at SEQ ID NO:1 are replaced by an amino acid sequence comprising $Xaa_n$, wherein n is from about 5 to about 21, and each Xaa is independently a random amino acid.

9. The polypeptide of claim 8 wherein the polypeptide further comprises a cell-permeant region fused to the amino terminal end of the polypeptide.

10. The polypeptide of claim 9 wherein the cell-permeant region comprises an amino acid sequence selected from the group consisting of YGRKKRRQRRR (SEQ ID NO:2), RQIKIWFQNRRMKWKK (SEQ ID NO:3), RQIKIWFPNRRMKWKK (SEQ ID NO:4), and RQPKIWFPNRRPKWKK (SEQ ID NO:5).

11. A cell comprising the polypeptide of claim 8.

12. A collection of polynucleotides comprising at least two polynucleotides, each polynucleotide comprising a coding sequence encoding a polypeptide comprising a fragment of SEQ ID NO:1 beginning at any amino acid from about 119 to about 124 and ending at any amino acid from about 262 to about 275, wherein at least two consecutive amino acids within the regions of amino acids 129-137, or amino acids 182-189, or amino acids 257-264 as depicted at

SEQ ID NO:1 are replaced by an amino acid sequence comprising $Xaa_n$, wherein n is from about 5 to about 21, and each Xaa is independently a random amino acid.

13. The collection of claim 12 wherein the polypeptide encoded by the coding sequence of each member of the collection further comprises a cell-permeant region fused to the amino terminal end of the polypeptide.

14. The collection of claim 13 wherein the cell-permeant region comprises an amino acid sequence selected from the group consisting of YGRKKRRQRRR (SEQ ID NO:2), RQIKIWFQNRRMKWKK (SEQ ID NO:3), RQIKIWFPNRRMKWKK (SEQ ID NO:4), and RQPKIWFPNRRPKWKK (SEQ ID NO:5).

15. The collection of claim 14 wherein the nucleotide sequence of the coding sequence encoding the $Xaa_n$ consists of a nucleotide sequence $NNK_m$, wherein N is independently a random nucleotide, K is independently a guanine or a thymine, and wherein o is from about 5 to about 21.

16. A vector comprising a member of the collection of claim 12.

17. The collection of claim 16 wherein the vector is a retrovirus.

18. A cell comprising a member of the collection of claim 12.

19. A population of cells comprising two or more cells, wherein each member of the population comprises one polynucleotide of the collection of claim 12.

20. A method for crystallizing a polypeptide comprising an amino acid sequence SEQ ID NO:1, the method comprising:

preparing purified polypeptide comprising an amino acid sequence SEQ ID NO:1 at a concentration of about 3 mg/ml to about 20 mg/ml; and

crystallizing the polypeptide comprising an amino acid sequence SEQ ID NO:1 from a solution comprising about 20 % by weight to about 28 % by weight polyethylene glycol, about 0.05 M to about 0.2 M ammonium sulfate, and about 1 mM to about 20 mM urea, wherein the solution is buffered to a pH of about 6 to about 8.

21. A method for crystallizing a polypeptide comprising an amino acid sequence SEQ ID NO:1, the method comprising:

preparing purified polypeptide comprising an amino acid sequence SEQ ID NO:1 at a concentration of about 3 mg/ml to about 20 mg/ml; and

crystallizing the polypeptide comprising an amino acid sequence SEQ ID NO:1 from a solution comprising about 15 % by weight to about 25 % by weight polyethylene glycol 4000, and about 0.05 M to about 0.4 M MgCl2, wherein the solution is buffered to a pH of about 6 to about 8.

22. A crystal of a polypeptide comprising an amino acid sequence SEQ ID NO:1.

23. The crystal of claim 22 having the space group symmetry $P2_12_12_1$.

24. The crystal of claim 22 comprising a unit cell having dimensions of a, b, and c; wherein a is about 69.3 Å to about 72.0 Å, b is about 75.2 Å to about 76.0 Å, and c is about 90.1 Å to about 94.7 Å; and wherein $\alpha = \beta = \gamma =$ about 90°.

25. (Amended) A method for identifying a polypeptide within a collection that prevents cell death after exposure to a pathogen or a toxin, the method comprising:

providing a cell comprising a polypeptide that is a member of a collection of polypeptides comprising at least two polypeptides, each polypeptide comprising a fragment of a Venezuelan equine encephalitis virus (VEE) virus capsid polypeptide [SEQ ID NO:1] beginning at any amino acid from about 119 to about 124 and ending at any amino acid from about 258 to about 275, wherein at least two consecutive amino acids within the regions of amino acids 129-137, or amino acids 182-189, or amino acids 257-264 [as depicted at SEQ ID NO:1] are replaced

by an amino acid sequence comprising $Xaa_n$, wherein n is from about 5 to about 21, and each Xaa is independently a random amino acid , and wherein amino acids 119-275 of the VEE virus capsid polypeptide are amino acids 1-156 of SEQ ID NO:1 [.];

exposing the cell to a pathogen or a toxin; and

determining whether the polypeptide prevents cell death, comprising:

incubating the cell under conditions such that the pathogen or the toxin kills a cell that does not comprise a polypeptide that prevents cell death after exposure to a pathogen or a toxin, wherein the presence of a cell that proliferates indicates the polypeptide prevents cell death after exposure to a pathogen or a toxin.

26. The method of claim 25 wherein the pathogen is selected from the group consisting of a virus and a microbe.

27. The method of claim 26 wherein the microbe is selected from the group consisting of a bacterium, a rickettsia, and a fungus.

28. The method of claim 25 wherein the toxin is a biological toxin.

29. The method of claim 25 wherein the toxin is a chemical toxin.

30. A method for identifying a polypeptide within a collection that binds a pathogen, a toxin, a polypeptide, or a polynucleotide, the method comprising:

providing a cell comprising a polypeptide that is a member of a collection of polypeptides comprising at least two polypeptides, each polypeptide comprising fragment of SEQ ID NO:1 beginning at any amino acid from about 119 to about 124 and ending at any amino acid from about 258 to about 275, wherein at least two consecutive amino acids within the regions of amino acids 129-137, or amino acids 182-189, or amino acids 257-264 as depicted at SEQ ID NO:1 are replaced by an amino acid sequence comprising $Xaa_n$, wherein n is from about 5 to about 21, and each Xaa is independently a random amino acid;

exposing the cell to a pathogen or a toxin; and

determining whether the polypeptide binds the pathogen or the toxin, comprising:

incubating the cell under conditions such that the pathogen or the toxin kills a cell that does not comprise the polypeptide, wherein the presence of a cell that proliferates indicates the polypeptide binds the pathogen, the toxin, a polypeptide, or a polynucleotide.

31. The method of claim 30 wherein the pathogen is selected from the group consisting of a virus and a microbe.

32. The method of claim 31 wherein the microbe is selected from the group consisting of a bacterium, a rickettsia, and a fungus.

33. The method of claim 30 wherein the agent is a biological toxin.

34. The method of claim 30 wherein the agent is a chemical toxin.